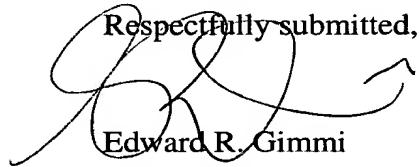


Patents, Mail Stop Sequence, P.O. Box 1450, Alexandria, Virginia 22313-1450, on 16 August 2004. As this response is being timely filed within the shortened statutory period for response of 1 months, no fee is required. Please charge any additional requisite fees relating to this response to Deposit Account No. 19-2570.

**REMARKS**

If it would expedite the prosecution of this application, the Examiner is invited to confer with the Applicants' undersigned attorney.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'E. Gimmi', is written over the typed name 'Edward R. Gimmi'.

Edward R. Gimmi  
Attorney for Applicants  
Registration No. 38,891

GLAXOSMITHKLINE  
Corporate Intellectual Property UW2220  
P.O. Box 1539  
King of Prussia, PA 19406-0939  
Phone (610) 270-4478  
Facsimile (610) 270-5090  
N:\ERG\APPS\Bcases\B45122\PREAMD4.DOC



**COPY**

CERTIFICATE OF MAILING

I HEREBY CERTIFY THAT THIS CORRESPONDENCE IS BEING DEPOSITED  
WITH THE UNITED STATES POSTAL SERVICE WITH SUFFICIENT POSTAGE  
AS FIRST-CLASS MAIL IN AN ENVELOPE ADDRESSED TO:  
COMMISSIONER FOR PATENTS, MAIL STOP SEQUENCE, P.O. BOX 1450,  
ALEXANDRIA, VA 22313-1450,

ON 16 AUGUST 2004

Debrah L. Pashley  
NAME OF PERSON MAILING DOCUMENTS

8/16/04  
DATE

Attorney Docket No.: B45122

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Bruck, *et al.*

16 August 2004

Serial No.: 09/554,860

Group Art Unit No.: 1644

Filed: 19 May 2000

Examiner: Patrick Nolan

For: Recombinant Allergen with Reduced Enzymatic Activity

**STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE  
WITH 37 CFR §§ 1.821 THROUGH 1.825**

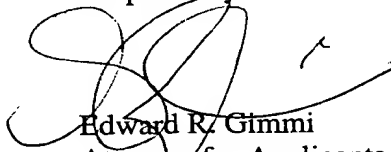
Commissioner for Patents  
Mail Stop Sequence  
P.O. Box 1450  
Alexandria, VA 22313-1450

- ( X ) I hereby state that the contents of the paper and computer readable copies of the Substitute Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.
- ( X ) I hereby state that the submission filed in accordance with 37 CFR §1.821 (g) does not include new matter.
- ( ) I hereby state that the submission filed in accordance with 37 CFR §1.821 (h) does not include new matter or go beyond the disclosure in the international application as filed.
- ( ) I hereby state that the amendments, made in accordance with 37 CFR §1.825 (a), included in the substitute sheet(s) of the Sequence Listing are supported in the application, as filed, at pages \_\_\_\_\_. I hereby state that the substitute sheet(s) of the Sequence Listing does (do) not include new matter.
- ( ) I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 CFR §1.825(b), is the same as the amended Sequence Listing.

Serial No.: 09/554,860  
Group Art Unit No.: 1644

( ) I hereby state that the substitute copy of the computer readable form, submitted in accordance with **37 CFR §1.825(d)**, is identical to that originally filed.

Respectfully submitted,



Edward R. Gimmi  
Attorney for Applicants  
Registration No. 38,891

GLAXOSMITHKLINE  
Corporate Intellectual Property - UW2220  
P.O. Box 1539  
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Phone (610) 270-4478  
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N:\ERG\APPS\Bcases\B45122\statsupp3.doc



UNITED STATES PATENT AND TRADEMARK OFFICE

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P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/554,860	05/19/2000	CLAUDINE BRUCK	B45122	6653

20462 7590 07/26/2004

SMITHKLINE BEECHAM CORPORATION  
CORPORATE INTELLECTUAL PROPERTY-US, UW2220  
P. O. BOX 1539  
KING OF PRUSSIA, PA 19406-0939



EXAMINER

NOLAN, PATRICK J

ART UNIT PAPER NUMBER

1644

DATE MAILED: 07/26/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

RECEIVED  
GLAXOSMITHKLINE  
2004 JUL 28 P 2:18



## UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS  
UNITED STATES PATENT AND TRADEMARK OFFICE  
WASHINGTON, DC 20231  
www.uspto.gov

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
---------------------------------	-------------	---	---------------------



EXAMINER
----------

ART UNIT	PAPER
----------	-------

20040722

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner of Patents

The communication filed 9-12-03 is not fully responsive to the Office communication mailed 8-19-03 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

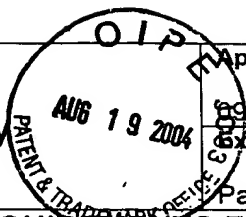
The fax number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Patrick Nolan whose telephone number is 571-272-0847.

If attempts to reach the examiner are unsuccessful, the examiner's supervisor, Christina Chan, can be reached at 571-272-0841.

*Pat J. Nolan*  
Patrick J. Nolan, Ph.D.  
Primary Examiner, Group 1640  
July 22, 2004

**Notice to Comply**

Application No.

59/554,860

Examiner

Patrick J. Nolan

Applicant(s)

BRUCK ET AL.

Art Unit

1644

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

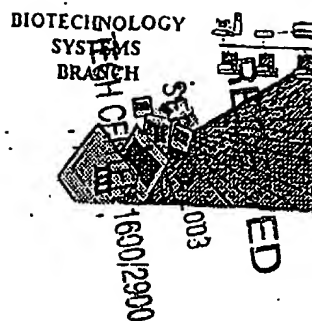
PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,860 A  
Source: 1600  
Date Processed by STIC: 9-22-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/554,860 A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>X</u> Use of <220>	Sequence(s) <u>31</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	





1600

## RAW SEQUENCE LISTING

DATE: 09/22/2003

PATENT APPLICATION: US/09/554,860A

TIME: 11:09:37

Input Set : A:\US seqlist2.txt

Output Set: N:\CRF4\09222003\I554860A.raw

4 <110> APPLICANT: Bruck, Claudine  
 5 Bollen, Alex  
 6 Jacobs, Paul  
 7 Massaer, Marc  
 9 <120> TITLE OF INVENTION: Recombinant Allergen with Reduced  
 10 Enzymatic Activity  
 12 <130> FILE REFERENCE: B45122  
 14 <140> CURRENT APPLICATION NUMBER: 09/554,860A  
 15 <141> CURRENT FILING DATE: 2000-05-19  
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP98/07521  
 18 <151> PRIOR FILING DATE: 1998-11-16  
 20 <150> PRIOR APPLICATION NUMBER: GB 9724531.0  
 21 <151> PRIOR FILING DATE: 1997-11-19  
 23 <160> NUMBER OF SEQ ID NOS: 30  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

**Does Not Comply  
Corrected Diskette Needed**

## ERRORED SEQUENCES

631 <210> SEQ ID NO: 31  
 632 <211> LENGTH: 4  
 633 <212> TYPE: PRT  
 634 <213> ORGANISM: Artificial Sequence  
 636 <220> FEATURE:  
 W--> 637 <221> NAME/KEY: Mutant of DerP1  
 E--> 639 <400> SEQUENCE: 31 - mandatory  
 639 Asn Ala Glu Thr  
 640 1

See item on error  
summary sheet.

response  
needed.

VERIFICATION SUMMARY

DATE: 09/22/2003

PATENT APPLICATION: US/09/554,860A

TIME: 11:09:39

Input Set : A:\US seqlist2.txt

Output Set: N:\CRF4\09222003\I554860A.raw

L:637 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31  
L:639 M:200 E: Mandatory Header Field missing, <400> is required.

# COPY

## SEQUENCE LISTING

<110> Bruck, Claudine  
Bollen, Alex  
Jacobs, Paul  
Massaer, Marc

<120> Recombinant Allergen with Reduced  
Enzymatic Activity

<130> B45122

<140> 09/554,860

<141> 2000-05-19

<150> PCT/EP98/07521

<151> 1998-11-16

<150> GB 9724531.0

<151> 1997-11-19

<160> 30

<170> FastSEQ for Windows Version 4.0

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<211> 963

<212> DNA

<213> Artificial Sequence

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<223> Mutant of DerP1

<400> 1

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<213> Artificial Sequence

<220>

<223> Mutant of DerP1

<400> 2

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Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
 35      40      45
Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
 50      55      60
Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
 65      70      75      80
Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
 85      90      95
Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile
100      105      110
Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly
115      120      125
Cys Gly Ser Ala Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala
130      135      140
Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu
145      150      155      160
Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg
165      170      175
Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr
180      185      190
Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg
195      200      205
Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys
210      215      220
Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile
225      230      235      240
Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile
245      250      255
Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr Ala Ala Val Asn Ile
260      265      270
Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn
275      280      285
Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala
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<223> Mutant of DerP1

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ttagacgcat tccgtcatta tgatggccga acaatcattc aacgcgataa tggttaccaa 780
ccaaactatc acgctgtcaa cattgttggg tacagtaacg cacaaggtgt cgattattgg 840
atcgtacgaa acagttggga taccaattgg ggtgataatg gttacggtta ttttgcgtgc 900
aacatcgtat tgatgatgat tgaagaatat ccatatgttg tcattctcta a 951

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<210> 4

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant of DerP1

<400> 4

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Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala
20     25     30
Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
35     40     45
Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
50     55     60
Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
65     70     75     80
Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
85     90     95
Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln
100    105    110
Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys
115    120    125
Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr
130    135    140
Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala
145    150    155    160

Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr
165    170    175
Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala
180    185    190
Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser
195    200    205
Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala
210    215    220
Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp
225    230    235    240

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Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	Arg	Asp
				245					250					255	
Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly	Tyr	Ser
			260					265					270		
Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	Asp	Thr
		275					280					285			
Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile	Asp	Leu
	290					295					300				
Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu				
305					310					315					

<210> 5  
 <211> 963  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant of DerP1

<400> 5  
 atgaaaattg ttttggccat cgcctcattg ttggcattga gcgctgttta tgctcgtcca 60  
 tcatcgatca aaacttttga agaatacaaa aaagccttca acaaaaagtta tgctaccttc 120  
 gaagatgaag aagctgcccg taaaaacttt ttggaatcag taaaatatgt tcaatcaaat 180  
 ggaggtgccca tcaaccattt gtccgatttg tcgttggatg aattcaaaaa ccgatttttg 240  
 atgagtgcag aagcttttga acacctcaaa actcaattcg atttgaatgc tgaaactaac 300  
 gcctgcagta tcaatggaaa tgctccagct gaaatcgatt tgcgacaaat gcgaactgtc 360  
 actcccattc gtatgcaagg aggctgtggt tcacgatggg ctttctctgg tgttgccgca 420  
 actgaatcag cttatttggc ttaccgtaat caatcattgg atcttgctga acaagaatta 480  
 gtcgattgtg cttcccaaca cggttgtcat ggtgatacca ttccacgtgg tattgaatac 540  
 atccaacata atggtgtcgt ccaagaaagc tactatcgat acgttgcacg agaacaatca 600  
 tgccgacgac caaatgcaca acgtttcggg atctcaaact attgccaaat ttaccaccca 660  
 aatgtaaaca aaattcgtga agctttggct caaaccacaca gcgctattgc cgtcattatt 720  
 ggcatacaag atttagacgc attccgtcat tatgatggcc gaacaatcat tcaacgcgat 780  
 aatggttacc aaccaaacta tgctgctgtc aacattgttg gttacagtaa cgcacaagg 840  
 gtcgattatt ggatcgtacg aaacagttgg gataccaatt ggggtgataa tggttacgg 900  
 tattttgctg ccaacatcga tttgatgatg attgaagaat atccatatgt tgctcattctc 960  
 taa 963

<210> 6  
 <211> 320  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant of DerP1

<400> 6  
 Met Lys Ile Val Leu Ala Ile Ala Ser Leu Leu Ala Leu Ser Ala Val  
 1 5 10 15  
 Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala  
 20 25 30  
 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys  
 35 40 45  
 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile  
 50 55 60

Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu
65					70					75					80
Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn
				85					90					95	
Ala	Glu	Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile
			100					105					110		
Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly
		115				120						125			
Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala
	130					135					140				
Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu
145					150					155					160
Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg
				165				170						175	
Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr
		180						185					190		
Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg
		195					200					205			
Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys
	210					215					220				
Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile
225					230					235					240
Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile
				245					250					255	
Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	Ala	Ala	Val	Asn	Ile
			260					265					270		
Val	Gly	Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn
		275					280					285			
Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala
	290					295					300				
Asn	Ile	Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu
305					310					315					320

<210> 7  
 <211> 339  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant of DerP1

Met	Leu	Leu	Val	Asn	Gln	Ser	His	Gln	Gly	Phe	Asn	Lys	Glu	His	Thr
1				5					10					15	
Ser	Lys	Met	Val	Ser	Ala	Ile	Val	Leu	Tyr	Val	Leu	Leu	Ala	Ala	Ala
			20					25					30		
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr
		35					40					45			
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu
	50					55					60				
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val
65					70					75					80

Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp
			85						90					95	

Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	
			100					105					110			
Lys	Thr	Gln	Phe	Asp	Leu	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	
		115					120					125				
Ala	Glu	Ile	Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	
		130				135					140					
Gln	Gly	Gly	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	
145					150					155					160	
Glu	Ser	Ala	Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	
			165					170						175		
Gln	Glu	Leu	Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	
			180					185					190			
Ile	Pro	Arg	Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	
		195					200					205				
Ser	Tyr	Tyr	Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	
	210					215					220					
Ala	Gln	Arg	Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	
225					230					235					240	
Ala	Asn	Lys	Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	
			245					250						255		
Val	Ile	Ile	Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	
		260					265						270			
Arg	Thr	Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala		
	275					280					285					
Val	Asn	Ile	Val	Gly	Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	
	290				295						300					
Val	Arg	Asn	Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	
305					310					315					320	
Phe	Ala	Ala	Asn	Ile	Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	
			325						330					335		
Val	Ile	Leu														

<210> 8  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant of DerP1

<400> 8

Met	Leu	Leu	Val	Asn	Gln	Ser	His	Gln	Gly	Phe	Asn	Lys	Glu	His	Thr	
1				5				10					15			
Ser	Lys	Met	Val	Ser	Ala	Ile	Val	Leu	Tyr	Val	Leu	Leu	Ala	Ala	Ala	
			20					25					30			
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr	
		35					40					45				
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu	
	50					55					60					
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val	
65					70					75					80	
Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	
			85					90					95			
Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	
			100					105					110			



Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn  
 115 120 125  
 Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr  
 130 135 140  
 Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Ala Trp Ala Phe Ser Gly  
 145 150 155 160  
 Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu  
 165 170 175  
 Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys  
 180 185 190  
 His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly  
 195 200 205  
 Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys  
 210 215 220  
 Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile  
 225 230 235 240  
 Tyr Pro Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His  
 245 250 255  
 Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg  
 260 265 270  
  
 His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro  
 275 280 285  
 Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val  
 290 295 300  
 Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn  
 305 310 315 320  
 Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu  
 325 330 335  
 Tyr Pro Tyr Val Val Ile Leu  
 340

<210> 9  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 9  
 tcgagaaaag agaggctgaa gctactaacg cctgca

36

<210> 10  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 10  
 ggcgtagta gcttcagcct ctcttttc

28

<210> 11  
 <211> 86

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 11  
gatccaaacg atgagatttc cttcaatttt tactgcagtt ttattcgcag catcctccgc 60  
attagctgct ccaactaacg cctgca 86

<210> 12  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 12  
ggcgtagtt ggagcagcta atgcggagga tgctgcgaat aaaactgcag taaaaattga 60  
aggaaatctc atcgtttg 78

<210> 13  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 13  
aattcaaaaa ccgatttttg atgagtgcag aagcttttga acacctaaaa ctcaattcga 60  
tttgaacgcc tgca 74

<210> 14  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 14  
ggcgttcaaa tcgaattgag ttttgaggtg ttcaaaagct tctgcatcat caaaaatcgg 60  
tttttg 66

<210> 15  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 15  
catgaaaatt gttttggcca tcgcc 25

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 16  
cggtttttga attcatccaa cgac

24

<210> 17  
<211> 113  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 17  
taatggaaat gctccagctg aaatcgattt gcgacaaatg cgaactgtca ctcccattcg 60  
tatgcaagga ggctgtggtt cagcttgggc tttctctggt gttgccgcaa ctg 113

<210> 18  
<211> 114  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 18  
attcagttgc ggcaacacca gagaaagccc aagctgaacc acagcctcct tgcatacgaa 60  
tgggagtgc agttcgcatt tgcgcaaat cgatttcagc tggagcattt ccat 114

<210> 19  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 19  
aattcaaaaa ccgatttttg atgagtgcag aagcttttga acacctcaaa actcaattcg 60  
atttgaacgc ctgca 75

<210> 20  
<211> 67  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 20  
ggcgttcaaa tcgaattgag ttttgaggtg ttcaaaagct tctgcactca tcaaaaatcg 60

gtttttg

67

<210> 21

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

catgaaaatt gttttggcca tcgcc

25

<210> 22

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

cggtttttga attcatccaa cgac

24

<210> 23

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

agcttaccat gaaaattggt ttggccatcg cctcattggt ggcattgagc gctgtttatg 60  
ctcgactaa cgctgca 78

<210> 24

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

ggcgtagta cgagcataaa cagcgctcaa tgccaacaat gaggcgatgg ccaaaacaat 60  
tttcatggta 70

<210> 25

<211> 172

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

gatccccggc cgtcatcgat caaaactttt gaagaataca aaaaagcctt caacaaaagt 60  
tatgctacct tcgaagatga agaagctgcc cgtaaaaact ttttggaatc agtaaaatat 120  
gttcaatcaa atggaggtgc catcaacccat ttgtccgatt tgcgttgga tg 172

<210> 26

<211> 172

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

aattcatcca acgacaaatc ggacaaatgg ttgatggcac ctccatttga ttgaacatat 60  
tttactgatt ccaaaaagtt ttacgggca gcttcttcat cttcgaaggt agcataactt 120  
ttgttgaagg cttttttgta ttcttcaaaa gttttgatcg atgacggccg gg 172

<210> 27

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27

gtacccttaa gatgcta 17

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 28

ctagtagcat cttaagg 17

<210> 29

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29

aattcaaaaa ccgatttttg atgagtgcag aagcttttga acacctcaaa actcaattcg 60  
atttgaacgc ctgca 75

<210> 30

<211> 67

<212> DNA

<213> Artificial Sequence

<220>